

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 14:52:59 : Search time 1133 Seconds  
(without alignments)  
1.687 Million cell updates/sec

Title: CER06C7  
Perfect score: 30911  
Sequence: 1 gaattcattctctggaacctg.....tttgcctcttcagcattctt 30911

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : 24-sep-2003-z71266.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30911	100.0	30911	1 CER06C7	ACCESSION:Z71266

## ALIGNMENTS

RESULT 1  
CER06C7 30911 bp DNA linear INV 24-SEP-2003  
Caenorhabditis elegans cosmid R06C7, complete sequence.  
Z71266  
Z71266.1 GI:1279324  
HTG: Adenylosuccinate lyase; Myosin heavy chain; Rat TOAD-64 protein like; Serine/threonine-protein kinase; Zinc finger protein.  
SOURCE  
Caenorhabditis elegans  
ORGANISM  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REMARK  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
none.  
Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium  
Science 282 (5396), 2012-2018 (1998)  
99069613  
9851916  
The *C. elegans* Sequencing Consortium.  
Gardner, A.E.  
2 (bases 1 to 30911)  
Direct Submission  
Submitted (19-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jesusanger.ac.uk or iw@nematode.wustl.edu

## COMMENT

Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.  
Current sequence finishing criteria for the *C. elegans* genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.  
IMPORTANT: This sequence is not the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.  
The true left end of clone R06C7 is at 1 in this sequence. The true right end of clone R06C7 is at 8718 in this sequence. The true left end of clone F21C3 is at 30808 in this sequence. The start of this sequence (1..106) overlaps with the end of sequence 298261.  
The end of this sequence (30808..30911) overlaps with the start of sequence 271261.  
For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=R06C7>  
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.  
Location/Qualifiers

## FEATURES

## source

## gene

## CDS

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CDs  
gene

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QY 5761 TTAATTAATCTCTTAACGCTTAACCTTTTCACTTCTGTTGCGGCGCAAGCCACTGAATGA 5820  
DB TTAATTAATCTCTTAACGCTTAACCTTTTCACTTCTGTTGCGGCGCAAGCCACTGAATGA 5820  
QY 5821 AATATTCCTCGGGGCTTGTCTTGGATTAACGCTGTGACAAATCCGCAATGTAAAGCGTTCT 5880  
DB AATATTCCTCGGGGCTTGTCTTGGATTAACGCTGTGACAAATCCGCAATGTAAAGCGTTCT 5880  
QY 5881 TCTCTGAAGGTCACAGACTCTTCAAGGAACAGCAAAACACATTTGATGATGCTGCTG 5940  
DB TCTCTGAAGGTCACAGACTCTTCAAGGAACAGCAAAACACATTTGATGATGCTGCTG 5940  
QY 5941 CTGAGACTGCAAAAGCTCAATGAGCCGCTGGAGAGCTGACTTCACTTTGTGTCATC 6000  
DB CTGAGACTGCAAAAGCTCAATGAGCCGCTGGAGAGCTGACTTCACTTTGTGTCATC 6000  
QY 6001 ATACCAATATTTTCCCTGAGCAGCTGATTTCCACTCCACTTATATGTGGCAATGAGT 6060  
DB ATACCAATATTTTCCCTGAGCAGCTGATTTCCACTCCACTTATATGTGGCAATGAGT 6060

QY 6061 ATGCAAGCGTGAAGAGATCTGCGGTGAACCTAACCTAGGTTTTTTGTTTAAAAACA 6120  
DB ATGCAAGCGTGAAGAGATCTGCGGTGAACCTAACCTAGGTTTTTTGTTTAAAAACA 6120  
QY 6121 AAAATTTATTTATATTTTTCAGAGACTAAAGCAATTTGAAGCAAGAGTCCGAAGCG 6180  
DB AAAATTTATTTATATTTTTCAGAGACTAAAGCAATTTGAAGCAAGAGTCCGAAGCG 6180  
QY 6181 AGCGCTCAAGAACTTTCAAAGGAATCGCTTACAAACCAACGATCTCAATCAAGAC 6240  
DB AGCGCTCAAGAACTTTCAAAGGAATCGCTTACAAACCAACGATCTCAATCAAGAC 6240  
QY 6241 GCGTCAATGCAATGATTTGAGCTATGACATACCTGATGTTTACGATGATTA 6300  
DB GCGTCAATGCAATGATTTGAGCTATGACATACCTGATGTTTACGATGATTA 6300  
QY 6301 ATTTTACGCTACCTAGAGATTAATTTTACGTTTCCGCTAGTTTATTTGTAATTTT 6360  
DB ATTTTACGCTACCTAGAGATTAATTTTACGTTTCCGCTAGTTTATTTGTAATTTT 6360  
QY 6361 TTAATCAATGTTTATATTTTGTATGATGCTGTGTGACCCGTAATTTAACTC 6420  
DB TTAATCAATGTTTATATTTTGTATGATGCTGTGTGACCCGTAATTTAACTC 6420  
QY 6421 GGTATGATTAAGTTTATGAGCTGATTAATTTTCAAGATTTGCTTGTGCGTAAAGT 6480  
DB GGTATGATTAAGTTTATGAGCTGATTAATTTTCAAGATTTGCTTGTGCGTAAAGT 6480  
QY 6481 TCGAGCGATGTTTTTGAAGATCTTCAAGTGAAGAAACGAAGTTGCTGATTAAGAGGG 6540  
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QY 6541 GAATTTTGTGATTTTTTTTGAATTTGAACATTAACATTTCTAAGCTGCTCCAA 6600  
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QY 6601 GTCAATGACTAGTGCATTAATATTTACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6660  
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QY 6661 ATTTATTCACGTTTAACTCAAAATGCTAATTCGAAAGTTAATCAGAAAGAAAGTA 6720  
DB ATTTATTCACGTTTAACTCAAAATGCTAATTCGAAAGTTAATCAGAAAGAAAGTA 6720  
QY 6721 ATTAATTAAGAAAGCAATTTCAATCAAGCTTTCAACATTCCTTGTGTAATTTCTGTC 6780  
DB ATTAATTAAGAAAGCAATTTCAATCAAGCTTTCAACATTCCTTGTGTAATTTCTGTC 6780  
QY 6781 CTTTTCGCTGAGTTGAAAAAAGCAATGCTGAATTCGCAAGAAAGGGAATTAATTTCC 6840  
DB CTTTTCGCTGAGTTGAAAAAAGCAATGCTGAATTCGCAAGAAAGGGAATTAATTTCC 6840  
QY 6841 AGATCCGGGAACGTTTGAAGTTTCCGTGAGCCCATCAATTCGCCCTCTGTAATAGT 6900  
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QY 6901 TGTGTTAATGTTGTCGCAATGAGAAATGCTGAAATPACAAAGATCAAACTTTTGG 6960  
DB TGTGTTAATGTTGTCGCAATGAGAAATGCTGAAATPACAAAGATCAAACTTTTGG 6960  
QY 6961 ATTATTTTATTTTATTTTTCATTTGAGCTGCGCTTCAAAATTAAGACGATTAATGAGCTGC 7020  
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QY 7021 GGAAGCTTCTTTCACCAATGTAAGAAATGCTATTTATGGAACACAAAAATTTGGAATG 7080  
DB GGAAGCTTCTTTCACCAATGTAAGAAATGCTATTTATGGAACACAAAAATTTGGAATG 7080  
QY 7081 CGTATGCAACAATCTTTGCGGCGCAAAATTCGTAAGCAAAACATGATATTTCTT 7140  
DB CGTATGCAACAATCTTTGCGGCGCAAAATTCGTAAGCAAAACATGATATTTCTT 7140  
QY 7141 TAAATGACTACTGTAGCGCTTACGACATCATTTAATAAATGATCAATAATATTAGAA 7200

D	b		7141	TAAATGACTCTAGCGCTTACGGACATCAATTAAATAATTCATCAAAATATTAGAA		7200	
Oy			7201	GAAAACCTTAAGCTACAAAAATATCCGTGCATATTCGAAAAAATTCATTTCAA		7260	
D	b		7201	GAAAACCTTAAGCTACAAAAATATCCGTGCATATTCGAAAAAATTCATTTCAA		7260	
Oy			7261	TCGAGCCCGTAATTCGACACAAGCGCTACAGTTGTAATTTAAAGAAATACAGAGTTTC		7320	
D	b		7261	TCGAGCCCGTAATTCGACACAAGCGCTACAGTTGTAATTTAAAGAAATACAGAGTTTC		7320	
Oy			7321	GCTAGAGATATTTGGCGCTCAATATGTTGCAATACGCCATTCGGAATTTTTTCT		7380	
D	b		7321	GCTAGAGATATTTGGCGCTCAATATGTTGCAATACGCCATTCGGAATTTTTTCT		7380	
Oy			7381	TCOCGTATTAACATTCGTTATATCTCATATTAAGATACAAATGTTTAAATCTGAACCTTA		7440	
D	b		7381	TCOCGTATTAACATTCGTTATATCTCATATTAAGATACAAATGTTTAAATCTGAACCTTA		7440	
Oy			7441	AATCCATTAAGTCGCGTACTATATATTTAGTATATTTGTACAGTAACCCCCCTCGAA		7500	
D	b		7441	AATCCATTAAGTCGCGTACTATATATTTAGTATATTTGTACAGTAACCCCCCTCGAA		7500	
Oy			7501	TTTTCCGATATTTTATTCAAAAATTTGTAATTAATCCTAAAGTTTGCTGCATTTTACA		7560	
D	b		7501	TTTTCCGATATTTTATTCAAAAATTTGTAATTAATCCTAAAGTTTGCTGCATTTTACA		7560	
Oy			7561	CCTACAGAACACATTTTCTAGCTCAATATTTGTTGAAAAAATATGCGGGAATTTT		7620	
D	b		7561	CCTACAGAACACATTTTCTAGCTCAATATTTGTTGAAAAAATATGCGGGAATTTT		7620	
Oy			7621	GAAATGTTTAAAGTTTTGTGTACGCGGTACTACATATTAAGACACATGCGCATGTCACAC		7680	
D	b		7621	GAAATGTTTAAAGTTTTGTGTACGCGGTACTACATATTAAGACACATGCGCATGTCACAC		7680	
Oy			7681	TTTCAAAAATCTTGTGCATATCAAAATATATTGTTGTTGTTCTGAAAAACCGAAAGATTC		7740	
D	b		7681	TTTCAAAAATCTTGTGTGCATATCAAAATATATTGTTGTTGTTCTGAAAAACCGAAAGATTC		7740	
Oy			7741	AAAAGTCTGACGATATATATATATATATATATGACTATATCTCTGAAAAAAGCTCGGAATA		7800	
D	b		7741	AAAAGTCTGACGATATATATATATATATATATGACTATATCTCTGAAAAAAGCTCGGAATA		7800	
Oy			7801	AAGSTTCAACGGAATTTGTAATATTTTAAACATATGCTGTAGAAGAACCAAACTTCGCGCA		7860	
D	b		7801	AAGSTTCAACGGAATTTGTAATATTTTAAACATATGCTGTAGAAGAACCAAACTTCGCGCA		7860	
Oy			7861	TCTAGGCTATTAACATATTTTGTCTGTACACAAATCTCACGAGAAATAGTAACCTTGGCAA		7920	
D	b		7861	TCTAGGCTATTAACATATTTTGTCTGTACACAAATCTCACGAGAAATAGTAACCTTGGCAA		7920	
Oy			7921	CTCCGTGACAGTTGATCTCTTCAAAAATGTTGAANTCGAGGTTCTGAAAAAGTTTGATAG		7980	
D	b		7921	CTCCGTGACAGTTGATCTCTTCAAAAATGTTGAANTCGAGGTTCTGAAAAAGTTTGATAG		7980	
Oy			7981	AAAAAGGGAAGATAGATCATACATAAACAATTTGTCATAGATTTCTTTAAAAATTA		8040	
D	b		7981	AAAAAGGGAAGATAGATCATACATAAACAATTTGTCATAGATTTCTTTAAAAATTA		8040	
Oy			8041	GTTGAAAAAAGATATATATCAAAATTCGAATATTAATTAACCAACATGATAGA		8100	
D	b		8041	GTTGAAAAAAGATATATATCAAAATTCGAATATTAATTAACCAACATGATAGA		8100	
Oy			8101	TGTTGTCTCTTTGAAATAGTCTAGTGGCATTTGATGAAAAATTAACAATATCTGCATCG		8160	
D	b		8101	TGTTGTCTCTTTGAAATAGTCTAGTGGCATTTGATGAAAAATTAACAATATCTGCATCG		8160	
Oy			8161	GAACCAACCTCAATTTCTTCCCTTCTGTGATTAATTTAAAAATTTTTCGACCTTTGAA		8220	
D	b		8161	GAACCAACCTCAATTTCTTCCCTTCTGTGATTAATTTAAAAATTTTTCGACCTTTGAA		8220	
Oy			8221	CTGGTTATTAAGACATATCTCATTTGATCAATTAATTCAGAAATGTAACCCCTTTTCCAT		8280	
D	b		8221	CTGGTTATTAAGACATATCTCATTTGATCAATTAATTCAGAAATGTAACCCCTTTTCCAT		8280	

QY 9361 AGTACGTTGAACATATTAAATTCCTCAATTCCTTGAAAGCAAGTTGTCAATTTA 9420  
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Db 9361 AGTACGTTGAACATATTAAATTCCTCAATTCCTTGAAAGCAAGTTGTCAATTTA 9420  
QY 9421 CCMAAATTTGCTGAAACAATTTCAATTCYAAAAAGAAATTTGAGTGTATATATGAT 9480  
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Db 9421 CCMAAATTTGCTGAAACAATTTCAATTCYAAAAAGAAATTTGAGTGTATATATGAT 9480  
QY 9481 ATTGAGATATTTTGGAAATGTTATATGCTGATTCAGTTATACACTTGCCTTAATTAAT 9540  
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Db 9481 ATTGAGATATTTTGGAAATGTTATATGCTGATTCAGTTATACACTTGCCTTAATTAAT 9540  
QY 9541 ATGAGTTACCTCTGTGGCTACCTGTGTATGTCTTCAGGCCAGTAACTCTTTGTC 9600  
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Db 9541 ATGAGTTACCTCTGTGGCTACCTGTGTATGTCTTCAGGCCAGTAACTCTTTGTC 9600  
QY 9601 CAATTAATCAATTTCTTTTCTTAAATCAGTAACCAATTTTCACAATGAACCTTGGCA 9660  
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Db 9601 CAATTAATCAATTTCTTTTCTTAAATCAGTAACCAATTTTCACAATGAACCTTGGCA 9660  
QY 9661 TGCCTAGATTTTGACATTCCTGTGATTCCTGAAATATATCATCTCTGACCATTTAG 9720  
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Db 9661 TGCCTAGATTTTGACATTCCTGTGATTCCTGAAATATATCATCTCTGACCATTTAG 9720  
QY 9721 TGTGTTCTCATTAAGCATGTAGAAATTTGACGAATTAACCTCCTTAATTAATTAATTT 9780  
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Db 9721 TGTGTTCTCATTAAGCATGTAGAAATTTGACGAATTAACCTCCTTAATTAATTAATTT 9780  
QY 9781 GAGATATTTTGTGTTTTGAAAAATTTATATTTTCAGAAATCTAATATATATCAACTAC 9840  
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Db 9781 GAGATATTTTGTGTTTTGAAAAATTTATATTTTCAGAAATCTAATATATATCAACTAC 9840  
QY 9841 AAATCTGACCTGTAAATATTCGCAATTCGATTCACACTTCTGTGCTCCACATGTGAT 9900  
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Db 9841 AAATCTGACCTGTAAATATTCGCAATTCGATTCGATTCACACTTCTGTGCTCCACATGTGAT 9900  
QY 9901 AGCAACTATAAACCATATATCAACAACACTTTTGATCTGCCAACTCTTCATCTATTT 9960  
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Db 9901 AGCAACTATAAACCATATATCAACAACACTTTTGATCTGCCAACTCTTCATCTATTT 9960  
QY 9961 GTACACGACATCAATGACTCCCAATTCCTATGATCCGGACAAAGAAATCAATATCTG 10020  
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Db 9961 GTACACGACATCAATGACTCCCAATTCCTATGATCCGGACAAAGAAATCAATATCTG 10020  
QY 10021 AAATTAACCTTTCTATTCATTTGATTCGATTTCTAAACCCGCCAGTTGATGGA 10080  
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Db 10021 AAATTAACCTTTCTATTCATTTGATTCGATTTCTAAACCCGCCAGTTGATGGA 10080  
QY 10081 GAAATATGACCTTGCAAAATGTGAGTGTATTCACCTTGTTAACAGGATATTTAA 10140  
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Db 10081 GAAATATGACCTTGCAAAATGTGAGTGTATTCACCTTGTTAACAGGATATTTAA 10140  
QY 10141 TATATTAATGATCTATGTATTAATTCGATTAATTTCAAAAAAGAAACGGGAAT 10200  
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Db 10141 TATATTAATGATCTATGTATTAATTCGATTAATTTCAAAAAAGAAACGGGAAT 10200  
QY 10201 TATAAAGAAGGATTTTTCGCTGACTTTAAAAATTAATTAATTTGCAAAAAAACTT 10260  
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Db 10201 TATAAAGAAGGATTTTTCGCTGACTTTAAAAATTAATTAATTTGCAAAAAAACTT 10260  
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QY 10321 AAATTAATTTGAAAGCATTTTATATTAATTCCTGTTGCGGGTTTGAAAGAAATCTGA 10380  
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QY 10381 AAACATAGATGAAGGCGGATCCGCTTTTTCGAAGTCTTCAAAAAAAACGGTTGTCA 10440

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Db 10441 ATTTAAGGATACTAATAAATCTTGATCCCTAGAAATAAACATTTTGTATAGGCA 10500  
QY 10501 CAACGTTTGGCGCATTTCTGAAATAGACCCCAATTTTGTAGCGAGGTAGCGACTACA 10560  
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Db 10501 CAACGTTTGGCGCATTTCTGAAATAGACCCCAATTTTGTAGCGAGGTAGCGACTACA 10560  
QY 10561 TCTATGCGATGAGCTTATTAATTTAATTCAGTAAGTATCTCACATTTGATGTTCCCGAC 10620  
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QY 10621 AACTGCTGCTCTGTTCCCTTCCAAAAAATCAATCTTTGCACTTCCCATTAATGAGAT 10680  
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QY 10681 TTGCATATGTGTAGAGATCAATACCTCCAGGAATCAAGACGATCGTTGCATCAAT 10740  
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Db 10681 TTGCATATGTGTAGAGATCAATACCTCCAGGAATCAAGACGATCGTTGCATCAAT 10740  
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Db 10741 TACTCTGATCTGTAGAGAGATATATTTTGGAGATATCTCTCGAATATGCTTTT 10800  
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Db 10981 TGAACAATATATTTAAATCATATTAATGAATTTAAAAATGCTGAAACACTTTTCAGTTGAT 11040  
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Db 11221 GAATTAAGATATTTTATTTATTCACCTATCACTTAATTTAACTTAACCTTA 11280  
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Db 11281 ACAGTTTTTACACGATCTCTGTTTGAACATTCACAAATTAATTCATTTCTCAAGGA 11340  
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QY 11521 ATATATGTTGTATGAAGAAATTAAGAAAGATACCGGGGCGTGTATGATTAAC 11580



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Db 11761 ATGACTTGTGGAAGATGTTGATTCACAGTGTGAGTCTTTCACATGACATGTTCT 11820  
Qy 11821 ACACATATGCCATCCGTCGCGCTCTTTCTATTAAAGCTTAAGCTTCATGTCGAAG 11880  
Db 11821 ACACATATGCCATCCGTCGCGCTCTTTCTATTAAAGCTTAAGCTTCATGTCGAAG 11880  
Qy 11881 AGAATGGAATGAGATGCTGACAAAGGTCCCTTCTGACAAAGAAACTAAATAGC 11940  
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Qy 12601 GATTTTATCTCACAAATGCAATTCACAAATTCAGTCTTCAATGATGTTTGGT 12660  
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Db 12721 AATGTTAACAATTTGACATCTCTGCTCAACCCAGCCGATCCGTCGCAAACTGT 12780  
Qy 12781 ATGTTTCCGCAAGTGAATGATGATTCACCGGAGATTCATCTGAGAAATTTCTGCGAGA 12840  
Db 12781 ATGTTTCCGCAAGTGAATGATGATTCACCGGAGATTCATCTGAGAAATTTCTGCGAGA 12840  
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Qy 13021 TCACCTTCAACAGTTGAGACACTCAACAGCTGATGCTTCAACAACTTCACTGATAC 13080  
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Qy 13081 AGAAGCTATTCACCAAGCTAATCTGTCATCTAGTGAATTTCTGACCCCTTTTA 13140  
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Qy 13141 ATTCATATTTTAAATCTTTAGATGATGCTCTCTGCTCAACGCTCAAACTCGGAA 13200  
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Qy 13201 TCTCTCTCAACATGCTGCTGCTCAACTCTCAGATGTTCTGAGAGTCTGCTTTTAC 13260  
Db 13201 TCTCTCTCAACATGCTGCTGCTCAACTCTCAGATGTTCTGAGAGTCTGCTTTTAC 13260  
Qy 13261 TCAATGAATGAAACGGAACCGGAACATCTGCAACAGTACTTTCATCTGCTG 13320  
Db 13261 TCAATGAATGAAACGGAACCGGAACATCTGCAACAGTACTTTCATCTGCTG 13320  
Qy 13321 TCTGCTATGAGATTTCTGATGTTGGAATGGAATAATGATGAGCTCTTCCGGAAT 13380  
Db 13321 TCTGCTATGAGATTTCTGATGTTGGAATGGAATAATGATGAGCTCTTCCGGAAT 13380  
Qy 13381 GCAACTGTAACTCTGCTCTTTGATGCGCGTAAGTTTCAATTTATTTGACAGAGAT 13440  
Db 13381 GCAACTGTAACTCTGCTCTTTGATGCGCGTAAGTTTCAATTTATTTGACAGAGAT 13440  
Qy 13441 TTTAAATATTTATTTTCAATGCGCAAGAGAGAGAGTCTTGGAGAGATTTCAACGGTGC 13500  
Db 13441 TTTAAATATTTATTTTCAATGCGCAAGAGAGAGAGTCTTGGAGAGATTTCAACGGTGC 13500  
Qy 13501 TTTGCAAGCAATTTCCGCTACTTGGATTTGTTTGGCTTCAACCAAGCAATCTCAC 13560  
Db 13501 TTTGCAAGCAATTTCCGCTACTTGGATTTGTTTGGCTTCAACCAAGCAATCTCAC 13560  
Qy 13561 TTTGCAAGCAATTTCCGCTACTTGGATTTGTTTGGCTTCAACCAAGCAATCTCAC 13620  
Db 13561 TTTGCAAGCAATTTCCGCTACTTGGATTTGTTTGGCTTCAACCAAGCAATCTCAC 13620  
Qy 13621 TGTGAGAGAGTCCAGAGATTTGCTATGCAATGAGATTTCTGTTTCTTAATGACCC 13680  
Db 13621 TGTGAGAGAGTCCAGAGATTTGCTATGCAATGAGATTTCTGTTTCTTAATGACCC 13680  
Qy 13681 ATCTTATGCGCTTTTATTTTATTTTGGCCAAATFATATTGCAACAAAGTTTACGATGAT 13740  
Db 13681 ATCTTATGCGCTTTTATTTTATTTTGGCCAAATFATATTGCAACAAAGTTTACGATGAT 13740



QY	13741	AAAAATTCA	TGATTTCTA	TTAACTTCA	CAACATTTGA	ATGAAATG	AAAAATCA	AAAAATCA	CT	13800
Db	13741	AAAAATTTCA	TGATTTCTA	TTAACTTCA	CAACATTTGA	ATGAAATG	AAAAATCA	AAAAATCA	CT	13800
QY	13801	TGGAATTA	TATTCGA	ACAGTTTCG	GTTCGTC	CAATACG	CTCGTTC	CGATTG	TTGTCTG	13860
Db	13801	TGGAATTA	TATTCGA	ACAGTTTCG	GTTCGTC	CAATACG	CTCGTTC	CGATTG	TTGTCTG	13860
QY	13861	ACATTCG	ATCAGTTC	CAATCAAA	TTTCGATG	TTTATG	AGAAATTT	TAATG	CCATTCAG	13920
Db	13861	ACATTCG	ATCAGTTC	CAATCAAA	TTTCGATG	TTTATG	AGAAATTT	TAATG	CCATTCAG	13920
QY	13921	GAGGTGC	CTTAGGTAT	CTCCATTC	CTCGAAAG	CAATATG	AGATCGAT	CGATG	AGAGCA	13980
Db	13921	GAGGTGC	CTTAGGTAT	CTCCATTC	CTCGAAAG	CAATATG	AGATCGAT	CGATG	AGAGCA	13980
QY	13981	AGGATATG	TATGATTTCT	CCCTCGGA	ATTTACAG	AAATTTTCTG	AGAAATTA	ATTTATTC	AAACCTG	14040
Db	13981	AGGATATG	TATGATTTCT	CCCTCGGA	ATTTACAG	AAATTTTCTG	AGAAATTA	ATTTATTC	AAACCTG	14040
QY	14041	AAGAAAA	AGTTAAAG	TGATGAC	ACCTCTG	AAATTTAG	TGTCAG	CGCTG	AGCATTTCTG	14100
Db	14041	AAGAAAA	AGTTAAAG	TGATGAC	ACCTCTG	AAATTTAG	TGTCAG	CGCTG	AGCATTTCTG	14100
QY	14101	CGAGATTC	ATCATGTTT	TTTCCCAAT	TATTTCTA	AGAAATCA	CAACATTC	CAATTC	GAGTGTAGAT	14160
Db	14101	CGAGATTC	ATCATGTTT	TTTCCCAAT	TATTTCTA	AGAAATCA	CAACATTC	CAATTC	GAGTGTAGAT	14160
QY	14161	CCAAATCG	TAGACTTTTG	ACCGCTTTT	TTCCTTTCA	ATGACAT	GACGTG	ATATCC		14220
Db	14161	CCAAATCG	TAGACTTTTG	ACCGCTTTT	TTCCTTTCA	ATGACAT	GACGTG	ATATCC		14220
QY	14221	AGGAAAC	ATGACAC	CGCTGA	AAATTAAT	TATGAAAT	CAATGAA	AAATTTCTG	TGATTTTAT	14280
Db	14221	AGGAAAC	ATGACAC	CGCTGA	AAATTAAT	TATGAAAT	CAATGAA	AAATTTCTG	TGATTTTAT	14280
QY	14281	TTATAAT	TATTAAT	CTTACTTG	ATGACTTTT	AGACGCTTT	TGTTC	CACAGT	GTGATACAT	14340
Db	14281	TTATAAT	TATTAAT	CTTACTTG	ATGACTTTT	AGACGCTTT	TGTTC	CACAGT	GTGATACAT	14340
QY	14341	TTACAGTC	GTTTGAT	TATTAAT	TGCGAAAT	TATTCAT	TTTAT	TCATCTA	TTTTC	14400
Db	14341	TTACAGTC	GTTTGAT	TATTAAT	TGCGAAAT	TATTCAT	TTTAT	TCATCTA	TTTTC	14400
QY	14401	AACCTTA	TATGACATTTT	CTTCTAC	CAATATG	CAAGATTTG	TATAC	ATGCTTCT	CGCCGCAATTC	14460
Db	14401	AACCTTA	TATGACATTTT	CTTCTAC	CAATATG	CAAGATTTG	TATAC	ATGCTTCT	CGCCGCAATTC	14460
QY	14461	ATTATGCT	TTAAATAT	TATGGAAT	TGGAAGG	AGAAATTC	CAATTTCA	AAAAAC	TTTATATCC	14520
Db	14461	ATTATGCT	TTAAATAT	TATGGAAT	TGGAAGG	AGAAATTC	CAATTTCA	AAAAAC	TTTATATCC	14520
QY	14521	CGAGATGA	ACGCGCAT	TGTAATTC	CGGATG	AAATGCG	ATATTTAT	TTATTC	TAATTC	14580
Db	14521	CGAGATGA	ACGCGCAT	TGTAATTC	CGGATG	AAATGCG	ATATTTAT	TTATTC	TAATTC	14580
QY	14581	AAGTGA	AAACAATTTT	TATCG	AGGATTTA	CTAATCT	ATTCAG	CAATTTAC	AAAAAATTC	14640
Db	14581	AAGTGA	AAACAATTTT	TATCG	AGGATTTA	CTAATCT	ATTCAG	CAATTTAC	AAAAAATTC	14640
QY	14641	ATTTAAGA	AAATGAT	CAAAATC	ACATCG	ACCTG	TCAGAT	TTATCA	AGATTC	14700
Db	14641	ATTTAAGA	AAATGAT	CAAAATC	ACATCG	ACCTG	TCAGAT	TTATCA	AGATTC	14700
QY	14701	TCAATTTG	TGGTTTCA	ATTTCTT	GGCAAT	TAAACCT	CTCGT	CTGG	AAAAACACACG	14760
Db	14701	TCAATTTG	TGGTTTCA	ATTTCTT	GGCAAT	TAAACCT	CTCGT	CTGG	AAAAACACACG	14760
QY	14761	GTGAAGTT	TATCG	GATTTAT	TGACAC	AGCCAC	ACAGCT	CGGAA	ACTG	14820
Db	14761	GTGAAGTT	TATCG	GATTTAT	TGACAC	AGCCAC	ACAGCT	CGGAA	ACTG	14820

[illegible]

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Db 15901 TTCATGAAAAAGCGGAGAGATCAATGACAGTTGGCAACGTTGTAAGATATGATCA 15960  
QY 15961 ATCGAATCGTAGGCAATAGATCAGATGTCTTGACAGACAGAAATAGCTCGG 16020  
Db 15961 ATCGAATCGTAGGCAATAGATCAGATGTCTTGACAGACAGAAATAGCTCGG 16020  
QY 16021 AGATGAATGATTCACAGCGCGCTTGCGGAGATTACCAAAAGCATGATTAGAGCCATC 16080  
Db 16021 AGATGAATGATTCACAGCGCGCTTGCGGAGATTACCAAAAGCATGATTAGAGCCATC 16080  
QY 16081 ACATATGCTTCAATTTTCTCTCTCGGATCGGATGAAAGGCCAATCGAATCATCTCTA 16140  
Db 16081 ACATATGCTTCAATTTTCTCTCTCGGATCGGATGAAAGGCCAATCGAATCATCTCTA 16140  
QY 16141 TTGGATTTTCATCTCAATTCATCTCATCTGATGATCTGTTTAAGACCGGACTCTTTTCA 16200  
Db 16141 TTGGATTTTCATCTCAATTCATCTCATCTGATGATCTGTTTAAGACCGGACTCTTTTCA 16200  
QY 16201 GCTTCAGCGAGCCAAATCCATAGTTGTCTCCAAAGAGTCGCTTATTAAGTCTCCGAGAG 16260  
Db 16201 GCTTCAGCGAGCCAAATCCATAGTTGTCTCCAAAGAGTCGCTTATTAAGTCTCCGAGAG 16260  
QY 16261 ATCGAAACAAAGTGGACTATCTTACAGTAAACGATGATGAAACCGACTCGAATCTGTCT 16320  
Db 16261 ATCGAAACAAAGTGGACTATCTTACAGTAAACGATGATGAAACCGACTCGAATCTGTCT 16320  
QY 16321 TCGGAGGCCATGATCAATTAACCTGAACCAAAAGCCTTAATTTTTCGAAATCTTCAAC 16380  
Db 16321 TCGGAGGCCATGATCAATTAACCTGAACCAAAAGCCTTAATTTTTCGAAATCTTCAAC 16380  
QY 16381 ATAAAACTGTAGAAATGTTTAAAGTATACACTAATACATAATAGATPAAGAAATGGCG 16440  
Db 16381 ATAAAACTGTAGAAATGTTTAAAGTATACACTAATACATAATAGATPAAGAAATGGCG 16440  
QY 16441 ATAACCATGAGAGAAAGATACAAAGAAACCATAAACGGAATAAAGTGAAGATCA 16500  
Db 16441 ATAACCATGAGAGAAAGATACAAAGAAACCATAAACGGAATAAAGTGAAGATCA 16500  
QY 16501 TGTTCGATAGGTGCAAAAAGAGTCAACCAATGATACACAGTAATTAATAAGGAATA 16560  
Db 16501 TGTTCGATAGGTGCAAAAAGAGTCAACCAATGATACACAGTAATTAATAAGGAATA 16560  
QY 16561 CCAATCCAAAGCGGAAAGTGTATATTAAGAGATCCTGATACGAATGAATATATGTAT 16620  
Db 16561 CCAATCCAAAGCGGAAAGTGTATATTAAGAGATCCTGATACGAATGAATATATGTAT 16620  
QY 16621 GTAGCTTTTATCAATAGTTGTACTTTTCGAGGTTGTAGACATACAGTCCGCTCAC 16680  
Db 16621 GTAGCTTTTATCAATAGTTGTACTTTTCGAGGTTGTAGACATACAGTCCGCTCAC 16680  
QY 16681 ACCATCTATCGGTAGAAATATCATGAGAGCTGAATAGATAGATTTTCATGAAATAATG 16740  
Db 16681 ACCATCTATCGGTAGAAATATCATGAGAGCTGAATAGATAGATTTTCATGAAATAATG 16740  
QY 16741 TCGTTCGCTCATGATTAACCTCACTCCACATCATACAGTTTCATCAAAATCTTCATCCAGC 16800  
Db 16741 TCGTTCGCTCATGATTAACCTCACTCCACATCATACAGTTTCATCAAAATCTTCATCCAGC 16800  
QY 16801 CGTGAATGTAGCATTTATAGTCTTTCATGATGATGATTTTCATCTAGCTGAGCAATAA 16860  
Db 16801 CGTGAATGTAGCATTTATAGTCTTTCATGATGATGATTTTCATCTAGCTGAGCAATAA 16860  
QY 16861 ACTGATTTTCAACATGTCAGAGAGCTTCAAGCGTAGTCTTACCTTAAACAGAGAAACA 16920  
Db 16861 ACTGATTTTCAACATGTCAGAGAGCTTCAAGCGTAGTCTTACCTTAAACAGAGAAACA 16920  
QY 16921 TTATGAATTAATTAATAGTGAACCAATCTCAACGATATTAACCAACCCGTTTGGAAA 16980  
Db 16921 TTATGAATTAATTAATAGTGAACCAATCTCAACGATATTAACCAACCCGTTTGGAAA 16980  
QY 16981 TCAGATTAACCTTAATTTGTCTATCTCTTGGGAAGCATTGGCTTGAACAGTCAA 17040  
Db 16981 TCAGATTAACCTTAATTTGTCTATCTCTTGGGAAGCATTGGCTTGAACAGTCAA 17040

Db 16981 TCAGATTAACCTTAATTTGTCTATCTCTTGGGAAGCATTGGCTTGAACAGTCAA 17040  
QY 17041 GGGGTAGGGTTCTGCACAAATTTCTTCTCCAACTATTCATCCATGATGATGTTCTCTTGA 17100  
Db 17041 GGGGTAGGGTTCTGCACAAATTTCTTCTCCAACTATTCATCCATGATGATGTTCTCTTGA 17100  
QY 17101 ACTCATTCGCGGCAACAGTTCCAAATTAATATCTTTCCGATACCACTGGGAGCAATA 17160  
Db 17101 ACTCATTCGCGGCAACAGTTCCAAATTAATATCTTTCCGATACCACTGGGAGCAATA 17160  
QY 17161 ATGTATTAATGATATGATATGAAACACGTCTTCAAGTGCATCTGGACATCCATCCCA 17220  
Db 17161 ATGTATTAATGATATGATATGAAACACGTCTTCAAGTGCATCTGGACATCCATCCCA 17220  
QY 17221 CAATAAGATATCCCTCAGTTTTCGAAATTTGAGATGGAACGAGCGTGGAGATTGGA 17280  
Db 17221 CAATAAGATATCCCTCAGTTTTCGAAATTTGAGATGGAACGAGCGTGGAGATTGGA 17280  
QY 17281 ATTGCTGAGCCAAAGGGTCTGATGAGCTCAAACTTTTGTCCAACTTAACTTTTCCAAA 17340  
Db 17281 ATTGCTGAGCCAAAGGGTCTGATGAGCTCAAACTTTTGTCCAACTTAACTTTTCCAAA 17340  
QY 17341 TCATGGGATCAATTTGGATCTTTTGTCTAATGATCAAAATGTACGTCGTGAGTATATC 17400  
Db 17341 TCATGGGATCAATTTGGATCTTTTGTCTAATGATCAAAATGTACGTCGTGAGTATATC 17400  
QY 17401 TTGGATTTTCCCATTTTATTTATGCTTGGCAATTTTATTTGTGCTCAATATATTCCT 17460  
Db 17401 TTGGATTTTCTCATTTTATTTATGCTTGGCAATTTTATTTGTGCTCAATATATTCCT 17460  
QY 17461 TTTTGCATTTAGTTGATATCCATGACTGCTGCAAAATCCAAACAGAAATATGAAGAAGC 17520  
Db 17461 TTTTGCATTTAGTTGATATCCATGACTGCTGCAAAATCCAAACAGAAATATGAAGAAGC 17520  
QY 17521 TTCCCTGCTATCCAAATTTGAGATCCAGAGCTTAACATTTGTGTCGATCTGAT 17580  
Db 17521 TTCCCTGCTATCCAAATTTGAGATCCAGAGCTTAACATTTGTGTCGATCTGAT 17580  
QY 17581 CTGAAGAGGATTCGGGAAAGTCTTCTTGTGATAGATACATTCCTGCTGCCACATA 17640  
Db 17581 CTGAAGAGGATTCGGGAAAGTCTTCTTGTGATAGATACATTCCTGCTGCCACATA 17640  
QY 17641 TTTCTTGAATTCGGCTACGGGTATTTCAATGAAATTTGAATTAATAGTTCAACAC 17700  
Db 17641 TTTCTTGAATTCGGCTACGGGTATTTCAATGAAATTTGAATTAATAGTTCAACAC 17700  
QY 17701 GTTGTCCAATTTGAAGAGATGCTGCTTGTAGAGAGCCCTCCCTCATCGAATTTGGAG 17760  
Db 17701 GTTGTCCAATTTGAAGAGATGCTGCTTGTAGAGAGCCCTCCCTCATCGAATTTGGAG 17760  
QY 17761 ACAGCGAAGTTTGGCCGACGATTTCCGATCAATGCAATTCGAAGTGTGAGATGATAT 17820  
Db 17761 ACAGCGAAGTTTGGCCGACGATTTCCGATCAATGCAATTCGAAGTGTGAGATGATAT 17820  
QY 17821 TAACATTAATTCGGAAGAAACAAACCTTACATTTACATTAATTTACATATCATTTTGGTA 17880  
Db 17821 TAACATTAATTCGGAAGAAACAAACCTTACATTTACATTAATTTACATATCATTTTGGTA 17880  
QY 17881 TTCTTCGTTGATTTGCAACGGCGGAGCATATACATTTTATCCATATTTGGATCTCAT 17940  
Db 17881 TTCTTCGTTGATTTGCAACGGCGGAGCATATACATTTTATCCATATTTGGATCTCAT 17940  
QY 17941 TCGGCGCTGAATTTCAAAATTTTACATTTATACAAATGTTTTCGAACTTTTAAATAGAT 18000  
Db 17941 TCGGCGCTGAATTTCAAAATTTTACATTTATACAAATGTTTTCGAACTTTTAAATAGAT 18000  
QY 18001 TGTTCCTAGATTTTATGTAACAGAACCATTAATTTATTTAGAAATAGTAAGAAGCTGGA 18060  
Db 18001 TGTTCCTAGATTTTATGTAACAGAACCATTAATTTATTTAGAAATAGTAAGAAGCTGGA 18060  
QY 18061 GCGTCAACCTTACTTTGGCAACCAACACATATCGTCGATTAATATTTGAGCCAAATTT 18120  
Db 18061 GCGTCAACCTTACTTTGGCAACCAACACATATCGTCGATTAATATTTGAGCCAAATTT 18120

QY	18121	CGTGTACGCTCCGATTAACCTAGACCGACGAACTGTATCCGCAAACTTTTTCATTTCGTGC	18180
Db	18121	CGTGTACGCTCCGATTAACCTAGACCGACGAACTGTATCCGCAAACTTTTTCATTTCGTGC	18180
QY	18181	AAACCATCTGACTGGATCGAATCGAGTCTTGATATACTAGACGACAGTTTTCGAA	18240
Db	18181	AAACCATCTGACTGGATCGAATCGAGTCTTGATATACTAGACGACAGTTTTCGAA	18240
QY	18241	CTACAAAAATTTGATTTTAAACCCGATTTACGAACAATATGAACCTACGATAACTCTTC	18300
Db	18241	CTACAAAAATTTGATTTTAAACCCGATTTACGAACAATATGAACCTACGATAACTCTTC	18300
QY	18301	CTTCAGCATTCCTTTAAATTAACGTGAAGTTAGATTCGATTCCTCACTCGAATGAA	18360
Db	18301	CTTCAGCATTCCTTTAAATTAACGTGAAGTTAGATTCGATTCGATTCCTCACTCGAATGAA	18360
QY	18361	AGAAAGTTTTCCTTTCGAGACGTAGATAATAGATTCGCCAACATAGCTTATACGAG	18420
Db	18361	AGAAAGTTTTCCTTTCGAGACGTAGATAATAGATTCGCCAACATAGCTTATACGAG	18420
QY	18421	TTTTCTGCTCCGATTTTGTGTACCTCGACAAATTTTCAGAAATTCAGACATCGAATTA	18480
Db	18421	TTTTCTGCTCCGATTTTGTGTACCTCGACAAATTTTCAGAAATTCAGACATCGAATTA	18480
QY	18481	AGACTGGTTTAAACGTAATTAGAGAAATGTTTATGAAATGAAAGTTAGTTCGATTT	18540
Db	18481	AGACTGGTTTAAACGTAATTAGAGAAATGTTTATGAAATGAAAGTTAGTTCGATTT	18540
QY	18541	GATTTGATTTTTCGAGGCTTGTCAAATTCACAGTGTACTCAATATCTCCAACTCAT	18600
Db	18541	GATTTGATTTTTCGAGGCTTGTCAAATTCACAGTGTACTCAATATCTCCAACTCAT	18600
QY	18601	TGATTCACACTGTCGTACTCAACCCGCTATACCTACGCGAAATTTCCATTTTTCGTAC	18660
Db	18601	TGATTCACACTGTCGTACTCAACCCGCTATACCTACGCGAAATTTCCATTTTTCGTAC	18660
QY	18661	AATTGTGCAGAAACACCCATAAGGCTCGAGCTTTCCAATTCATTCATCGATGCGCGT	18720
Db	18661	AATTGTGCAGAAACACCCATAAGGCTCGAGCTTTCCAATTCATTCATCGATGCGCGT	18720
QY	18721	CCTGATGAAAAATTTTCTTTCGAGCAACATATGCACTAGCTCCAGAGATGCTCTCAT	18780
Db	18721	CCTGATGAAAAATTTTCTTTCGAGCAACATATGCACTAGCTCCAGAGATGCTCTCAT	18780
QY	18781	CGCGATCCCAAAAAGTATTCGCATCGCTTCCCAATCGCACACTGTTAATTGGAAACACTT	18840
Db	18781	CGCGATCCCAAAAAGTATTCGCATCGCTTCCCAATCGCACACTGTTAATTGGAAACACTT	18840
QY	18841	CATCAAAATACACTTATACCTGACGCGCAACAGAAATCTTGTGCAGACTGACTGTATGT	18900
Db	18841	CATCAAAATACACTTATACCTGACGCGCAACAGAAATCTTGTGCAGACTGACTGTATGT	18900
QY	18901	AGAACACGCGAAGCACAAAATGACTAATTTTAGCAATTTTGGATGTCGGGAAGTACTT	18960
Db	18901	AGAACACGCGAAGCACAAAATGACTAATTTTAGCAATTTTGGATGTCGGGAAGTACTT	18960
QY	18961	TCGGACGACAAAAACACTCTTAAGTATCTGTGTACAAATTTAGACTACGTGGGCACGCTA	19020
Db	18961	TCGGACGACAAAAACACTCTTAAGTATCTGTGTACAAATTTAGACTACGTGGGCACGCTA	19020
QY	19021	ACTTCATTTATTTTCGAAACATTTTGTCTTAAAAAAAAGAAACAACAGAAAAATGGA	19080
Db	19021	ACTTCATTTATTTTCGAAACATTTTGTCTTAAAAAAAAGAAACAACAGAAAAATGGA	19080
QY	19081	GAAAAATGTTGAAAAATATATAAAAAGAAATGAGAGCTCAATGACATCCGTGCAATTC	19140
Db	19081	GAAAAATGTTGAAAAATATATAAAAAGAAATGAGAGCTCAATGACATCCGTGCAATTC	19140
QY	19141	GAAACATGAGCAAGCGACTACGAAAAAATGGCGGGCTTTTGTGTTATTTAAAAAGTGT	19200
Db	19141	GAAACATGAGCAAGCGACTACGAAAAAATGGCGGGCTTTTGTGTTATTTAAAAAGTGT	19200
QY	19201	GAACATGAGCAAGCGACTACGAAAAAATGGCGGGCTTTTGTGTTATTTAAAAAGTGT	19260
Db	19201	GAACATGAGCAAGCGACTACGAAAAAATGGCGGGCTTTTGTGTTATTTAAAAAGTGT	19260
QY	19261	ATTTCAAATGACTTTTAAATCAATTTTTCAGTTATAGCAATATTAAGACACCGCCCAATTTTCA	19320
Db	19261	ATTTCAAATGACTTTTAAATCAATTTTTCAGTTATAGCAATATTAAGACACCGCCCAATTTTCA	19320
QY	19321	GTAGTCCGCAATTTCTCGAGTTCAAAAGAACGTAGCCATGAGATGAGTCACTGAACCTA	19380
Db	19321	GTAGTCCGCAATTTCTCGAGTTCAAAAGAACGTAGCCATGAGATGAGTCACTGAACCTA	19380
QY	19381	CAGCGAAAAACCGCTCTATGAGCAGGCCCGGCAAGACTCGCTTTTCAAAAAAGACGC	19440
Db	19381	CAGCGAAAAACCGCTCTATGAGCAGGCCCGGCAAGACTCGCTTTTCAAAAAAGACGC	19440
QY	19441	CGCGTTTATATCCATTTCTGTTTTCGAAAGTCCCTAAATTTTACAGAGAAAGGAGATT	19500
Db	19441	CGCGTTTATATCCATTTCTGTTTTCGAAAGTCCCTAAATTTTACAGAGAAAGGAGATT	19500
QY	19501	TCACGCTTCCAATGAACCTCCGTAATTTTTCGTAACCGCATGATTTTATTTTCGGCTCTT	19560
Db	19501	TCACGCTTCCAATGAACCTCCGTAATTTTTCGTAACCGCATGATTTTATTTTCGGCTCTT	19560
QY	19561	TCCTACTTTGAAAACTTGTATTTCAGATTATTTCGAAAGTTATGTCCCATTTAGACTGG	19620
Db	19561	TCCTACTTTGAAAACTTGTATTTCAGATTATTTCGAAAGTTATGTCCCATTTAGACTGG	19620
QY	19621	CATTGCGTCCACTGACACCAACCTCCGACATGATGGCTTGAAGCTTGGCAACGCTAAG	19680
Db	19621	CATTGCGTCCACTGACACCAACCTCCGACATGATGGCTTGAAGCTTGGCAACGCTAAG	19680
QY	19681	TTTTCCGTATATCTGTATTTTAAATAGTACACACTTTTCAGGCAAAATCGATTCTCTC	19740
Db	19681	TTTTCCGTATATCTGTATTTTAAATAGTACACACTTTTCAGGCAAAATCGATTCTCTC	19740
QY	19741	AAATGATGACCGCGGAGAGAAATGAAGCGGGAATTTATACAGCTGCTTATAGAGAAATTTTC	19800
Db	19741	AAATGATGACCGCGGAGAGAAATGAAGCGGGAATTTATACAGCTGCTTATAGAGAAATTTTC	19800
QY	19801	GGGAGCAAAAGTTTGATCAAAATTCGTGAAAAAGAAAGGATCTCCGCTCTACAAAGTTA	19860
Db	19801	GGGAGCAAAAGTTTGATCAAAATTCGTGAAAAAGAAAGGATCTCCGCTCTACAAAGTTA	19860
QY	19861	TGGGTGACTAGTACAAACCTGAAGGGAGAGGCAATTTATGAACAACTTTTCAAAAAG	19920
Db	19861	TGGGTGACTAGTACAAACCTGAAGGGAGAGGCAATTTATGAACAACTTTTCAAAAAG	19920
QY	19921	ATCATTTACCTGTGTTCCGTGAAGTTCTATCTGCAATGGCGAGAAATGTGCAAAAATC	19980
Db	19921	ATCATTTACCTGTGTTCCGTGAAGTTCTATCTGCAATGGCGAGAAATGTGCAAAAATC	19980
QY	19981	AAATGCTGAGAGAAATTCAA	20040
Db	19981	AAATGCTGAGAGAAATTCAA	20040
QY	20041	TAGAAATGACAGCAATGGAATCGGGATTTCCGATTTGGTCGATGAATACTCAATGAG	20100
Db	20041	TAGAAATGACAGCAATGGAATCGGGATTTCCGATTTGGTCGATGAATACTCAATGAG	20100
QY	20101	AATCTGGAATATGTTCCACAGCCGATGAGACTATGGAATCTTTTCAGATTCAAATCGG	20160
Db	20101	AATCTGGAATATGTTCCACAGCCGATGAGACTATGGAATCTTTTCAGATTCAAATCGG	20160
QY	20161	GTTCTTAAGAAAAAGCGTCTCTTCGTTTCCCTTTTTCGAAACAATGTCCTTAATAATA	20220
Db	20161	GTTCTTAAGAAAAAGCGTCTCTTCGTTTCCCTTTTTCGAAACAATGTCCTTAATAATA	20220
QY	20221	ACTCGGGAAGAGCTGCATTTTGACCCAAAAGTAAGTTTGAAAAAAGTATATTTCTCAT	20280
Db	20221	ACTCGGGAAGAGCTGCATTTTGACCCAAAAGTAAGTTTGAAAAAAGTATATTTCTCAT	20280
QY	20281	TGGAACCTTATAGCCAAAGGGAATCTTTCGCAAGCTGTATGCGCAGGCCAAATATCAT	20340

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QY 22501 AACATGGCTGCTGTTGTGAGAGAAAGTATGCACAGTTGACTGAGCTAGCTTGGAGA 22560  
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Db 22501 AACATGGCTGCTGTTGTGAGAGAAAGTATGCACAGTTGACTGAGCTAGCTTGGAGA 22560  
22561 CTATTCGTTAAATGTCGACATCAAGAGGCGCAACATTCCTGGCGATGCTTCTAGATGT 22620  
|||||  
Db 22561 CTATTCGTTAAATGTCGACATCAAGAGGCGCAACATTCCTGGCGATGCTTCTAGATGT 22620  
QY 22621 CATTAACAGATTCTCTCAACATCCCTGCTGTGATTCACCTCCGACCTGGAAATTCCTGAT 22680  
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Db 22621 CATTAACAGATTCTCTCAACATCCCTGCTGTGATTCACCTCCGACCTGGAAATTCCTGAT 22680  
QY 22681 CAAGCTTTCTCGGAAATCTGGAATGAAAAGTTGGAAGCATCGGGATGGGACGGCGGT 22740  
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Db 22681 CAAGCTTTCTCGGAAATCTGGAATGAAAAGTTGGAAGCATCGGGATGGGACGGCGGT 22740  
QY 22741 TTCCAAAGTTCAAATGAGGCGCTGTGANTCTTGCCGACCAACAAAGTAGCCCAACACATGAA 22800  
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Db 22741 TTCCAAAGTTCAAATGAGGCGCTGTGANTCTTGCCGACCAACAAAGTAGCCCAACACATGAA 22800  
QY 22801 TTTGTAATTCGTCGCTTATGCTCTCTTTATGTCCTTTTGTGATGATCATGTGAAT 22860  
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Db 22801 TTTGTAATTCGTCGCTTATGCTCTCTTTATGTCCTTTTGTGATGATCATGTGAAT 22860  
QY 22861 AAACCTGTTGAGACTTTAATTAATGTCATCTAATTTATTTGCTAATAACAAATGAA 22920  
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Db 22861 AAACCTGTTGAGACTTTAATTAATGTCATCTAATTTATTTGCTAATAACAAATGAA 22920  
QY 22921 TTTAAAGCAAGTTTTACGTTTTTGAAGCTTTCCAAATTTGAGCTGATATTGCGATTTGG 22980  
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Db 22921 TTTAAAGCAAGTTTTACGTTTTTGAAGCTTTCCAAATTTGAGCTGATATTGCGATTTGG 22980  
QY 22981 GCGGGGAGAGCCCATACGCTAGAAATTTGATGCGCTTTAAAGGGAAGTATGCAATA 23040  
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Db 22981 GCGGGGAGAGCCCATACGCTAGAAATTTGATGCGCTTTAAAGGGAAGTATGCAATA 23040  
QY 23041 GATCACAGTTAGATCTAAATAGTGCACATTCGTTTTGTTCATCACTGTTTTCTTCCG 23100  
|||||  
Db 23041 GATCACAGTTAGATCTAAATAGTGCACATTCGTTTTGTTCATCACTGTTTTCTTCCG 23100  
QY 23101 GTTTTGCATAAATGTGATATTAAAAAGAAATTTAGAAAAAATTTACATTTAAAAATTT 23160  
|||||  
Db 23101 GTTTTGCATAAATGTGATATTAAAAAGAAATTTAGAAAAAATTTACATTTAAAAATTT 23160  
QY 23161 TCCGACATCCTCTGTAAAAATGGAAGAAATCAGATCAGACTGTGTGAGCGCTAGTGT 23220  
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Db 23161 TCCGACATCCTCTGTAAAAATGGAAGAAATCAGATCAGACTGTGTGAGCGCTAGTGT 23220  
QY 23221 TAATCAACTTATTTTGGAAAAAGTTTCAAGTTTTACCAAAATGTGAAAAATTAATTTGGCA 23280  
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Db 23221 TAATCAACTTATTTTGGAAAAAGTTTCAAGTTTTACCAAAATGTGAAAAATTAATTTGGCA 23280  
QY 23281 GTTTTATCATGACATGCTGTGATGAATAATGCTTGCATATCAAAAGCAATTTTGCAGC 23340  
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Db 23281 GTTTTATCATGACATGCTGTGATGAATAATGCTTGCATATCAAAAGCAATTTTGCAGC 23340  
QY 23341 AAGCTTACCTGACCAATCTTGGTATTTATCTTCATGTAAGCACTCAACATTAAGTTAG 23400  
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Db 23341 AAGCTTACCTGACCAATCTTGGTATTTATCTTCATGTAAGCACTCAACATTAAGTTAG 23400  
QY 23401 AGTTGTAGACTTAAAGGTGCGCATTCACATCTTCAAGTCAAGAGGAATTTGAATTAAG 23460  
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Db 23401 AGTTGTAGACTTAAAGGTGCGCATTCACATCTTCAAGTCAAGAGGAATTTGAATTAAG 23460  
QY 23461 TTGAAATCAGAGATCCAAAGCATGAATGCAAGATGAGGTGAATATTAATTTGGTAAA 23520  
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Db 23461 TTGAAATCAGAGATCCAAAGCATGAATGCAAGATGAGGTGAATATTAATTTGGTAAA 23520  
QY 23521 AATGCTGTATTAATTTTGGAAATTCAGAGCAATATCTTTCAATTTTGGAAAAATTCGCGAG 23580  
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Db 23521 AATGCTGTATTAATTTTGGAAATTCAGAGCAATATCTTTCAATTTTGGAAAAATTCGCGAG 23580

QY 23581 TTCACTAACCAAGCTGATGGCTCATTTTCTGGGAATTAATGCTTCATGTATGTAATAA 23640  
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Db 23581 TTCACTAACCAAGCTGATGGCTCATTTTCTGGGAATTAATGCTTCATGTATGTAATAA 23640  
QY 23641 CCAACTGTAAATTCATTTTCTTAATGAACATTTTTCAGGACAAAGCGTCCATATCATTAAC 23700  
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Db 23641 CCAACTGTAAATTCATTTTCTTAATGAACATTTTTCAGGACAAAGCGTCCATATCATTAAC 23700  
QY 23701 TGTGAAACACTATGTTGTGAGAGTGTGATACACTTAAATTAATGTCAGACAGTAGCG 23760  
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Db 23701 TGTGAAACACTATGTTGTGAGAGTGTGATACACTTAAATTAATGTCAGACAGTAGCG 23760  
QY 23761 ATGAACCCGATGAAGATATGCAAGAAAGACGACCCCGAGGAACCGGACGTCGGGTA 23820  
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Db 23761 ATGAACCCGATGAAGATATGCAAGAAAGACGACCCCGAGGAACCGGACGTCGGGTA 23820  
QY 23821 GTAAATTTGACATCGAAGACCCCTCTGCCAAATATTGAGACAAAAGAGAGAGATCCAAATTG 23880  
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Db 23821 GTAAATTTGACATCGAAGACCCCTCTGCCAAATATTGAGACAAAAGAGAGATCCAAATTG 23880  
QY 23881 TTAATTCGTCGGTTAGTTTCATTTTATGTTCTATATCTCATTTCTGTGTAATTAACAAAAAC 23940  
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Db 23881 TTAATTCGTCGGTTAGTTTCATTTTATGTTCTATATCTCATTTCTGTGTAATTAACAAAAAC 23940  
QY 23941 CTTCACATTAATTCACATTAATTAACCATATACATTAATTAATTAATTAATTAATTAATTAAT 24000  
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Db 23941 CTTCACATTAATTCACATTAATTAACCATATACATTAATTAATTAATTAATTAATTAATTAAT 24000  
QY 24001 AGTGTACCAACCATCAAAATTTCTCAAAATCTAAAGCATTAATTCGAACATGATTTT 24060  
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Db 24001 AGTGTACCAACCATCAAAATTTCTCAAAATCTAAAGCATTAATTCGAACATGATTTT 24060  
QY 24061 ATTCTCAATTCAGTGTGCTCAATATGTGATGCCAAATTTTAAACCATTCGTCGCTCTT 24120  
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Db 24061 ATTCTCAATTCAGTGTGCTCAATATGTGATGCCAAATTTTAAACCATTCGTCGCTCTT 24120  
QY 24121 GATCATGCTCAATCAAGAAACATTCACCTGAAAGATATGATGATGCTGTGCTGTGAGAAA 24180  
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Db 24121 GATCATGCTCAATCAAGAAACATTCACCTGAAAGATATGATGATGCTGTGCTGTGAGAAA 24180  
QY 24181 GAGTTTTGGAAGGACACATATCTATTTGCTATGATGCAAGAAATACAAAGTATATCAT 24240  
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Db 24181 GAGTTTTGGAAGGACACATATCTATTTGCTATGATGCAAGAAATACAAAGTATATCAT 24240  
QY 24241 TGTGACGTTGCAATTAATGCTTTGCGACGAAATGGCACTGGAAGACATCGATGTAG 24300  
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Db 24241 TGTGACGTTGCAATTAATGCTTTGCGACGAAATGGCACTGGAAGACATCGATGTAG 24300  
QY 24301 GAAATGGAACATTCGAGATTAATAAAGAAAGACGGGACGTGTAATGCGGAGAA 24360  
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Db 24301 GAAATGGAACATTCGAGATTAATAAAGAAAGACGGGACGTGTAATGCGGAGAA 24360  
QY 24361 ATAAAGTAAATTAATAAAGAGATTCAGATGCAAGAAATTTGGTGGCTTTTCTTAAT 24420  
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Db 24361 ATAAAGTAAATTAATAAAGAGATTCAGATGCAAGAAATTTGGTGGCTTTTCTTAAT 24420  
QY 24421 GAGATCATGAAAAATCAAAAGAGACCGTTTCCAAATTCGTTGTGATTTATGGAAG 24480  
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Db 24421 GAGATCATGAAAAATCAAAAGAGACCGTTTCCAAATTCGTTGTGATTTATGGAAG 24480  
QY 24481 AAATATCAACACTATTCATTTGCTCTCAAAACATATGAACCAAAATCTTGGAAACAGGAC 24540  
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Db 24481 AAATATCAACACTATTCATTTGCTCTCAAAACATATGAACCAAAATCTTGGAAACAGGAC 24540  
QY 24541 GAAATTCAGGTGGAGATGTTTATGAAACGTTTTTGGGAGACTTCACTAATTTGAAAT 24600  
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Db 24541 GAAATTCAGGTGGAGATGTTTATGAAACGTTTTTGGGAGACTTCACTAATTTGAAAT 24600  
QY 24601 ATAAAGTAAATTAACAGATTTTCTTTCTTTTAAACAAAAAATTAATTTTCAAGCA 24660  
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Db 24601 ATAAAGTAAATTAACAGATTTTCTTTCTTTTAAACAAAAAATTAATTTTCAAGCA 24660  
QY 24661 GAGATGGGACATTAACATTTGTTTGAAGAAATTCAGTGCATGTTTGTACCGAAGATA 24720  
|||||

Db 24661 GAGATGGACATTAACATGTTTGGCAGGAATTCAGGCAATGTTGGCTACCGAAGATA 24720  
Qy 24721 CAATTCGAGTTTGGTTCGAACGCCACATGGAAGAAGTGAATTCATCTACTGCACTCC 24780  
Db 24721 CAATTCGAGTTTGGTTCGAACGCCACATGGAAGAAGTGAATTCATCTACTGCACTCC 24780  
Qy 24781 TCCTGCGCTTTAGATCAAAACCATPAAGCTGCCAAACTGTGCATAAAAATATCAAAATGA 24840  
Db 24781 TCCTGCGCTTTAGATCAAAACCATPAAGCTGCCAAACTGTGCATAAAAATATCAAAATGA 24840  
Qy 24841 AATATGTTGATATATCAAGAAAGCAATGTCAGACATTAATCTCAGCTCTTCTGATGT 24900  
Db 24841 AATATGTTGATATATCAAGAAAGCAATGTCAGACATTAATCTCAGCTCTTCTGATGT 24900  
Qy 24901 ACATTTGGATGTCAACTCGTTGCGGAGACAGACCAAGTGAAGAGATCAGCTGCT 24960  
Db 24901 ACATTTGGATGTCAACTCGTTGCGGAGACAGACCAAGTGAAGAGATCAGCTGCT 24960  
Qy 24961 TCCTGATGTCATATTTATTTGGTATAGAACTGAAAGAGACAGCAATGACATGACGA 25020  
Db 24961 TCCTGATGTCATATTTATTTGGTATAGAACTGAAAGAGACAGCAATGACATGACGA 25020  
Qy 25021 AGATGCTGATGCTACATTCATCTCATCTTCCAGCTGGAATTTGGCATATTTCC 25080  
Db 25021 AGATGCTGATGCTACATTCATCTCATCTTCCAGCTGGAATTTGGCATATTTCC 25080  
Qy 25081 GGTAGATTAATCTTCTTCTTAAATCTTTTGGTGAACATCTTCTTCAATAT 25140  
Db 25081 GGTAGATTAATCTTCTTCTTAAATCTTTTGGTGAACATCTTCTTCAATAT 25140  
Qy 25141 CATGCTTTAAATATTAATATATCCACCAAGATTAATTAATTAATTAATTAATTAATTA 25200  
Db 25141 CATGCTTTAAATATTAATATATCCACCAAGATTAATTAATTAATTAATTAATTAATTA 25200  
Qy 25201 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25260  
Db 25201 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25260  
Qy 25261 CAATATTTGCGGCAAAAATGATTTCTATGAAAAATGAAAAATGAAAAATGAAAAAG 25320  
Db 25261 CAATATTTGCGGCAAAAATGATTTCTATGAAAAATGAAAAATGAAAAATGAAAAAG 25320  
Qy 25321 TATCATTAATGTTTACAAAATTTGAAGCTCTAATATGTTGTTCTTACATTAATTAATTT 25380  
Db 25321 TATCATTAATGTTTACAAAATTTGAAGCTCTAATATGTTGTTCTTACATTAATTAATTT 25380  
Qy 25381 AGTGTTCATGCTGGAAGTCTGTGCGGTGTTGGAAGTCTTCAATCATGAGGAAGC 25440  
Db 25381 AGTGTTCATGCTGGAAGTCTGTGCGGTGTTGGAAGTCTTCAATCATGAGGAAGC 25440  
Qy 25441 AAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25500  
Db 25441 AAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25500  
Qy 25501 TAACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25560  
Db 25501 TAACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25560  
Qy 25561 GCCGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25620  
Db 25561 GCCGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25620  
Qy 25621 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25680  
Db 25621 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25680  
Qy 25681 GAGCAACTTTGGCAAAATTTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 25740  
Db 25681 GAGCAACTTTGGCAAAATTTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 25740  
Qy 25741 ACGTATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 25800  
Db 25741 ACGTATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 25800

Db 25741 ACGTATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 25800  
Qy 25801 ATACAAATGAGCCGCTTGAGAGAAAAATACATCCCGTGTGCTAGATTCGAATA 25860  
Db 25801 ATACAAATGAGCCGCTTGAGAGAAAAATACATCCCGTGTGCTAGATTCGAATA 25860  
Qy 25861 CTCGAGAGAAATGAGCGTTTGTAAATTTCTTAATTAATTAATTAATTAATTAATTAATTA 25920  
Db 25861 CTCGAGAGAAATGAGCGTTTGTAAATTTCTTAATTAATTAATTAATTAATTAATTAATTA 25920  
Qy 25921 TAAATTCAGTCCGAGATGTCAGCGCTCTTATACCGTCGAGGCGTGTGTCATAT 25980  
Db 25921 TAAATTCAGTCCGAGATGTCAGCGCTCTTATACCGTCGAGGCGTGTGTCATAT 25980  
Qy 25981 CGACACGAATCTCAGGAGAAAAAAGAAATGTTCAATGCAACAACTGTTGAAACCTTCCA 26040  
Db 25981 CGACACGAATCTCAGGAGAAAAAAGAAATGTTCAATGCAACAACTGTTGAAACCTTCCA 26040  
Qy 26041 AACTATGCTGCTCTCCATGATCATTAATGATGATGATGATGATGATGATGATGATGATGAT 26100  
Db 26041 AACTATGCTGCTCTCCATGATCATTAATGATGATGATGATGATGATGATGATGATGATGAT 26100  
Qy 26101 CACATATGCTACACATGACCGCATTCGAGGACATPAATGATCAAAATGAAACAACTA 26160  
Db 26101 CACATATGCTACACATGACCGCATTCGAGGACATPAATGATCAAAATGAAACAACTA 26160  
Qy 26161 CGAGAGATATTCGAGAGAGACATCAATTAATGATGATGATGATGATGATGATGATGATGATG 26220  
Db 26161 CGAGAGATATTCGAGAGAGACATCAATTAATGATGATGATGATGATGATGATGATGATGATG 26220  
Qy 26221 TCGTAGAAGAAAGTGAATTTTCAATTCCTATTCACCGCATTTTTCGAGAAAGTATGATTA 26280  
Db 26221 TCGTAGAAGAAAGTGAATTTTCAATTCCTATTCACCGCATTTTTCGAGAAAGTATGATTA 26280  
Qy 26281 TTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26340  
Db 26281 TTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26340  
Qy 26341 AAATTTTGAAGCTGTCTCTTCTAGATTTAAACCTTCTCAATTAACCTCATGTTTACT 26400  
Db 26341 AAATTTTGAAGCTGTCTCTTCTAGATTTAAACCTTCTCAATTAACCTCATGTTTACT 26400  
Qy 26401 ATTAATTCGTTCTTCAACATTCACACAGAGAAAAAGTGTGATTTCTTACCAAGCAAG 26460  
Db 26401 ATTAATTCGTTCTTCAACATTCACACAGAGAAAAAGTGTGATTTCTTACCAAGCAAG 26460  
Qy 26461 GGAATTCCTGAAAAAACCAGCGGCAACCCGACTACTGATGATGATGATGATGATGATG 26520  
Db 26461 GGAATTCCTGAAAAAACCAGCGGCAACCCGACTACTGATGATGATGATGATGATGATG 26520  
Qy 26521 ATCTGCTGTCTTATCATCATTTTGTGAGAGTAAATAGAAAAAGAAAGAAAGAAAG 26580  
Db 26521 ATCTGCTGTCTTATCATCATTTTGTGAGAGTAAATAGAAAAAGAAAGAAAGAAAG 26580  
Qy 26581 ATTGATATTAATCAATGAGAGCTTAATTAACCTTTCTGAAAAAGAAAGTGTATG 26640  
Db 26581 ATTGATATTAATCAATGAGAGCTTAATTAACCTTTCTGAAAAAGAAAGTGTATG 26640  
Qy 26641 ATGATGATGACAGACACACCGTTTGCCTTTTGTGAATTTGATTTTCTAGAGCCTGG 26700  
Db 26641 ATGATGATGACAGACACACCGTTTGCCTTTTGTGAATTTGATTTTCTAGAGCCTGG 26700  
Qy 26701 GGCCTTTTGAAGGCGATTTACTGATTAATGATGAGGCTGATCCCTAGAAATCGAAG 26760  
Db 26701 GGCCTTTTGAAGGCGATTTACTGATTAATGATGAGGCTGATCCCTAGAAATCGAAG 26760  
Qy 26761 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26820  
Db 26761 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26820  
Qy 26821 GAAATCAACGAATTTAAAGATCAACGAGACCTGCGGCGCGAATCTGTTCAACACAGAG 26880  
Db 26821 GAAATCAACGAATTTAAAGATCAACGAGACCTGCGGCGCGAATCTGTTCAACACAGAG 26880



QY	26681	TGAGAGATATGTATTGAGACTGAAACTTTAAACAATTAGAAAAAGAAACCTGAAAAAC	26940
Db	26881	TGAGAGAAATTTGATTTAGACTGAAACTTTAAACAATTAGAAAAAGAAACCTGAAAAAC	26940
QY	26941	TTGATTTTAAACAAGATATGTGGGGGAAAAATACAAAACATATGAGAAATTTATTTGTGTG	27000
Db	26941	TTGATTTTAAACAAGATATGTGGGGGAAAAATACAAAACATATGAGAAATTTATTTGTGTGTG	27000
QY	27001	CACGACTGCTGAAAAAGATGATGAGACGAGAGAAGAAAAATCGACGAGAGCTTTGAAAGT	27060
Db	27001	CACGACTGCTGAAAAAGATGATGAGACGAGAGAAGAAAAATCGACGAGAGCTTTGAAAGT	27060
QY	27061	CAATGGGGGAAGTAAAGTTTTGTGTGTGTGGGGACCATGGAATTTATTCAGGGGGCAATTT	27120
Db	27061	CAATGGGGGAAGTAAAGTTTTGTGTGTGTGGGGACCATGGAATTTATTCAGGGGGCAATTT	27120
QY	27121	ACTGTGTGGTAGGCGGAACGACAACTTGACCGGGGACGTGGCAACAAATGTTCTCGGGCA	27180
Db	27121	ACTGTGTGGTAGGCGGAACGACAACTTGACCGGGGACGTGGCAACAAATGTTCTCGGGCA	27180
QY	27181	CCTCGGGACGCTCTTCGCGCATTCGAGACGCGAGTGTGATCTGTGGGAATTTGACAGAT	27240
Db	27181	CCTCGGGACGCTCTTCGCGCATTCGAGACGCGAGTGTGATCTGTGGGAATTTGACAGAT	27240
QY	27241	TCGTGGGTGGCGACCTCTCTCTCGTAAATTCAAACTTTTACTTTTGTAAATAATTTGAA	27300
Db	27241	TCGTGGGTGGCGACCTCTCTCTCGTAAATTCAAACTTTTACTTTTGTAAATAATTTGAA	27300
QY	27301	AAAAAAACAACATTTTACGACACCTTGAGAACTTTGAGAACTCATTTTGGTATTCGAATTCAT	27360
Db	27301	AAAAAAACAACATTTTACGACACCTTGAGAACTTTGAGAACTCATTTTGGTATTCGAATTCAT	27360
QY	27361	GAAGACGTGAACATTAATCTTTAAAGGACACGCGAGTTTTTAAAGTTGGTCTCGGCACGA	27420
Db	27361	GAAGACGTGAACATTAATCTTTAAAGGACACGCGAGTTTTTAAAGTTGGTCTCGGCACGA	27420
QY	27421	CCCTCTTATATTCAGTGCACCTACTATGATCAATAGTTGTAACCTATACATATTAAGTCAA	27480
Db	27421	CCCTCTTATATTCAGTGCACCTACTATGATCAATAGTTGTAACCTATACATATTAAGTCAA	27480
QY	27481	TAATGGCATTAATGATGAAACAAAGTTTAAAGATCGTATCCAAATATGATTCCAATTGGA	27540
Db	27481	TAATGGCATTAATGATGAAACAAAGTTTAAAGATCGTATCCAAATATGATTCCAATTGGA	27540
QY	27541	AATTCCAATTTGAACTAAATAGGTACTATTTGAATAAACTTTTGAAGTTGAAAAACAG	27600
Db	27541	AATTCCAATTTGAACTAAATAGGTACTATTTGAATAAACTTTTGAAGTTGAAAAACAG	27600
QY	27601	GAATGATTAATCGGATCAATTAAGTTTCAATATATATGTTAAACATTCGATCGCTGAT	27660
Db	27601	GAATGATTAATCGGATCAATTAAGTTTCAATATATATGTTAAACATTCGATCGCTGAT	27660
QY	27661	AATTCGCTAATATTCGTTGAGGTTTTAGTTAATAAAGTATACATACCGGCTCTGCA	27720
Db	27661	AATTCGCTAATATTCGTTGAGGTTTTAGTTAATAAAGTATACATACCGGCTCTGCA	27720
QY	27721	TTTGTCTCTTTTGGACGCGAATCTTCTGTGGAATTTGAAGCTTCGAGAGCTCTCTGAT	27780
Db	27721	TTTGTCTCTTTTGGACGCGAATCTTCTGTGGAATTTGAAGCTTCGAGAGCTCTCTGAT	27780
QY	27781	CGAAGCGCTCTTGTCTCTCTCGACACTTGGAAATTGAAGCTCACGAGCGGCTCTCTGCT	27840
Db	27781	CGAAGCGCTCTTGTCTCTCTCGACACTTGGAAATTGAAGCTCACGAGCGGCTCTCTGCT	27840
QY	27841	TGGGTATACCTTGTATGAGACTCTTGTGTGTCTGGCTGTCTCAAGTACCACTCGGCTTCCA	27900
Db	27841	TGGGTATACCTTGTATGAGACTCTTGTGTGTCTGGCTGTCTCAAGTACCACTCGGCTTCCA	27900
QY	27901	GGCTAGCAACAGATCTCTGACCTTGGCCAATGCTTTGGCACCGAGTGAATATACAAAT	27960
Db	27901	GGCTAGCAACAGATCTCTGACCTTGGCCAATGCTTTGGCACCGAGTGAATATACAAAT	27960

QY	27961	TTTGCAGCTTAGAATACCTTTGTTTGGTAACATACATTTGCATATGACATGGCAGCTTCACATCA	28020
Db	27961	TTTGCAGCTTAGAATACCTTTGTTTGGTAACATACATTTGCATATGACATGGCAGCTTCACATCA	28020
QY	28021	TCGATCTTAAAGCCAAATCTCTTGGCGGTAGAGCTGAGAGGAAATTGGGCTGTCGTGCGACA	28080
Db	28021	TCGATCTTAAAGCCAAATCTCTTGGCGGTAGAGCTGAGAGGAAATTGGGCTGTCGTGCGACA	28080
QY	28081	TGACATGCATGCTCTTCTTCTTGACGAGACCTCTTTCAGCAAGACAGATCCGCATACAGACT	28140
Db	28081	TGACATGCATGCTCTTCTTCTTGACGAGACCTCTTTCAGCAAGACAGATCCGCATACAGAGCT	28140
QY	28141	GCCTTGGCGGACGCTCCTCTTGAAAGCCTTAAGCTGCTCAAGTACTGCTCAATTCGTTTC	28200
Db	28141	GCCTTGGCGGACGCTCCTCTTGAAAGCCTTAAGCTGCTCAAGTACTGCTCAATTCGTTTC	28200
QY	28201	TGAAAGTTTATTTTTTAAATCTGACAAATCCCTTTAATAAATCTCATCTGCGCAATTCGA	28260
Db	28201	TGAAAGTTTATTTTTTAAATCTGACAAATCCCTTTAATAAATCTCATCTGCGCAATTCGA	28260
QY	28261	ACACGTCTTCAACCTTCTCTTCATGACGCAAGAAAGACAGATGTTTCCATTAAGCTCA	28320
Db	28261	ACACGTCTTCAACCTTCTCTTCATGACGCAAGAAAGACAGATGTTTCCATTAAGCTCA	28320
QY	28321	GTTTGGAAAGACTTGAAGTTCAGGCTGTTTCGATTTTCGAGTTTCTTATGCTTATCAGAT	28380
Db	28321	GTTTGGAAAGACTTGAAGTTCAGGCTGTTTCGATTTTCGAGTTTCTTATGCTTATCAGAT	28380
QY	28381	GCCTTCGATGCGGTCAGCAAGATCCTGCTTTTCAGAAAGACATACCAAGTCTCTTCTCA	28440
Db	28381	GCCTTCGATGCGGTCAGCAAGATCCTGCTTTTCAGAAAGACATACCAAGTCTCTTCTCA	28440
QY	28441	GCAGCAAAATGTTCTTCACGGATCTCCTCAAGCTCGTGATTCGCATATCAGATGCTGCT	28500
Db	28441	GCAGCAAAATGTTCTTCACGGATCTCCTCAAGCTCGTGATTCGCATATCAGATGCTGCT	28500
QY	28501	TGAAGTTCCTTGAACCTTGGTGCAGAAAGTTTCTTCAAGTCTTTCGGGCGTCAACGTTAGCC	28560
Db	28501	TGAAGTTCCTTGAACCTTGGTGCAGAAAGTTTCTTCAAGTCTTTCGGGCGTCAACGTTAGCC	28560
QY	28561	TTTGTGGCATATCCAAAGCAATCTGCAGTTGATGATGTCATCTCAAGCTTCAGGCTTCCTTG	28620
Db	28561	TTTGTGGCATATCCAAAGCAATCTGCAGTTGATGATGTCATCTCAAGCTTCAGGCTTCCTTG	28620
QY	28621	GCTCGGGGACCTCGGCGCTGCTGCTTCAGTTGCGGTTTCGAGGAGACCTTGGATGGACTCG	28680
Db	28621	GCTCGGGGACCTCGGCGCTGCTGCTTCAGTTGCGGTTTCGAGGAGACCTTGGATGGACTCG	28680
QY	28681	AGGGACAGTTCATGTTCTTTCGAGAGTTCCTGCAATTCCTCTCTTCTTCTTGAATCTTC	28740
Db	28681	AGGGACAGTTCATGTTCTTTCGAGAGTTCCTGCAATTCCTCTCTTCTTCTTGAATCTTC	28740
QY	28741	TTTCTGCATTTCTGAACGATCTGTTGAACCTGCATTTGAAGACGGAACCTTGGCTCTCT	28800
Db	28741	TTTCTGCATTTCTGAACGATCTGTTGAACCTGCATTTGAAGACGGAACCTTGGCTCTCTCT	28800
QY	28801	TCGGCTTCAATGACGCTCGGCGCTCATCAAGACAGATGTTGAAGCTGCTGCTCTTCTTCTCT	28860
Db	28801	TCGGCTTCAATGACGCTCGGCGCTCATCAAGACAGATGTTGAAGCTGCTGCTCTTCTTCTCT	28860
QY	28861	TCGAGACGGCGACAGACTTGTGAACCTTGTGTATGTACGTCCTTCTTGGGCTGATTTGTC	28920
Db	28861	TCGAGACGGCGACAGACTTGTGAACCTTGTGTATGTACGTCCTTCTTGGGCTGATTTGTC	28920
QY	28921	TCGTTAATGTCGCAATCTCTTGCAGAAAGATCTTGTCTCGCGCTCAAGGCTTCGATTT	28980
Db	28921	TCGTTAATGTCGCAATCTCTTGCAGAAAGATCTTGTCTCGCGCTCAAGGCTTCGATTT	28980
QY	28981	TGCTTCGCTGAGAGTTCCTCATGATGAAACGAAGTTTGAAGACCTTCAAGTATTTACGG	29040
Db	28981	TGCTTCGCTGAGAGTTCCTCATGATGAAACGAAGTTTGAAGACCTTCAAGTATTTACGG	29040
QY	29041	CTGTACAGAGTACGATCAATCTCTTTTGGATATCATCAACCTTCTCTTCCAGTCA	29100



Db	29041	CTGACAGAGTACGTGGGATCAATCTCTTTTGGATATCAATCAACCTTTCTCTTCCAGTCA	29100
QY	29101	TCAACGATCTGTGTCGAAAGCACGTGTCTTTTTCATGAGGGAAGCAATGACATCAAGTCA	29160
Db	29101	TCAACGATCTGTGTCGAAAGCACGTGTCTTTTTCATGAGGGAAGCAATGACATCAAGTCA	29160
QY	29161	CGATCAACATCTGAAGAGGATCTGGTTGCGCAAGAAAGTTTCCCTGGCCCTTCG	29220
Db	29161	CGATCAACATCTGAAGAGGATCTGGTTGCGCAAGAAAGTTTCCCTGGCCCTTCG	29220
QY	29221	AGAGAGATGACCTTGTCTCTGAGCAGAGAAGAAAGCCTCTTGAAGATCATCACTCTGTTC	29280
Db	29221	AGAGAGATGACCTTGTCTCTGAGCAGAGAAGAAAGCCTCTTGAAGATCATCACTCTGTTC	29280
QY	29281	ATCTGCTTTCTCTTGAGCTCTTCCAACTCCTCAAGATCCAACCAATCCTTCTCTCGTAT	29340
Db	29281	ATCTGCTTTCTCTTGAGCTCTTCCAACTCCTCAAGATCCAACCAATCCTTCTCTCGTAT	29340
QY	29341	CTGGCCTTTCATGAGAAATCTGGAAATGATACGGGAAAGTTGACGTTGAATGTCGCT	29400
Db	29341	CTGGCCTTTCATGAGAAATCTGGAAATGATACGGGAAAGTTGACGTTGAATGTCGCT	29400
QY	29401	TTTCCGTTGATTTGCTCTCTGACCAACTCGTGGCATTTGATCGAGTTTCTGTCTCAAGTTC	29460
Db	29401	TTTCCGTTGATTTGCTCTCTGACCAACTCGTGGCATTTGATCGAGTTTCTGTCTCAAGTTC	29460
QY	29461	TTTGACGACACATGGAACCTTTCACGCTGCTGAAGCTCGTCATTCACAGGACCTTCTTAAGCC	29520
Db	29461	TTTGACGACACATGGAACCTTTCACGCTGCTGAAGCTCGTCATTCACAGGACCTTCTTAAGCC	29520
QY	29521	TCTACAAAGTTGAGAGAAGAAATGCAATCTTGGCACGGGTGATGAGGCCAATGAATCTTCG	29580
Db	29521	TCTACAAAGTTGAGAGAAGAAATGCAATCTTGGCACGGGTGATGAGGCCAATGAATCTTCG	29580
QY	29581	AGCCTTCACCTTGAGCAGCAACAATGGGAGTTGCTGTGGAAGAAAGTTCCCTGGTGGAA	29640
Db	29581	AGCCTTCACCTTGAGCAGCAACAATGGGAGTTGCTGTGGAAGAAAGTTCCCTGGTGGAA	29640
QY	29641	GTTGACTCTCCGATTTTGTCTCGAGTTGCTGTCAACCTTTTGTGGAAGCTCGGCAACTTGG	29700
Db	29641	GTTGACTCTCCGATTTTGTCTCGAGTTGCTGTCAACCTTTTGTGGAAGCTCGGCAACTTGG	29700
QY	29701	ATTTCGTAATGCTTGGGAAGACCTTCTGTTCAACACGAGACTTGGTCTCTTGATCAAC	29760
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 23, 2003, 06:28:11 : Search time 14 Seconds

(without alignments)  
2.199 Million cell updates/sec

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Searched: 1 segs, 30911 residues

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Post-processing: Minimum Match 0%  
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Listing first 1 summaries

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Database: 23-jul-1999-z71266:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

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ACCESSION Z71266  
VERSION 271266.1 GI:1279324  
KEYWORDS HTG; Aenylosuccinate lyase; Myosin heavy chain; Rat TOAD-64  
SOURCE Protein Like; Serine/threonine-protein Kinase; Zinc finger protein.  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
Rhabditidae; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 30911)

#### REFERENCE

WILSON, R., AINSWORTH, R., ANDERSON, K., BAYNES, C., BERKS, M.,  
BONFIELD, J., BURTON, J., CONNELL, M., COPESEY, T., COOPER, J.,  
COUNLSON, A., CRAXTON, M., DEAR, S., DU, Z., DUTBIN, R., FAVELLO, A.,

TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,  
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Wilkinson-Spratt, J. and Wohldman, P.  
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans  
Nature 368 (6466), 32-38 (1994)  
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2 (bases 1 to 30911)  
Gardner, A.  
Submitted (19-APR-1996) Louis, MO 63110, USA. E-mail:  
jesse@sanger.ac.uk or twenematode.wustl.edu  
Coding sequences below are predicted from computer analysis, using  
predictions from GeneFINDER (P. Green, U. Washington), and other  
available information.  
For a graphical representation of this sequence and its analysis  
see:-  
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bin/display?db=wormaceclass=Sequence&object=R06C7  
Current sequence finishing criteria for the C. elegans genome  
sequencing consortium are that all bases are either sequenced  
unambiguously on both strands, or on a single strand with both a  
dye primer and dye terminator reaction, from distinct subclones.  
Exceptions are indicated by an explicit note.  
IMPORTANT: This sequence is NOT necessarily the entire insert of  
the specified clone. It may be shorter because we only sequence  
overlapping sections once, or longer because we arrange for a small  
overlap between neighbouring submissions.  
IMPORTANT: This sequence is not the entire insert of clone R06C7.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
The true left end of clone R06C7 is at 1 in this sequence. The true  
right end of clone R06C7 is at 8718 in  
sequence Z71261.  
The true left end of clone F21C3 is at 30808 in this sequence. The  
start of this sequence (1..106) overlaps with the end of sequence  
Z98261.  
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#### FEATURES

source

gene

CDS



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
4.024 Million cell updates/sec

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Listing first 1 summaries

Database : 23-jul-1999-z71266.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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ACCESSION Z71266  
VERSION 271266.1 GI:1279324  
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REFERENCE  
AUTHORS Wilson, R., Almscough, R., Anderson, K., Baynes, C., Berks, M.,  
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,  
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,  
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,  
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O Callaghan, M., Parsons, J., Percy, C., Riken, L., Roopra, A.,  
Saunders, D., Showkeen, R., Smalton, N., Smith, A., Sonhammer, E.,  
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaadin, M.,  
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Wilkinson-Sproat, J. and Wobldman, P.

TITLE  
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elegans  
Nature 368 (6466), 32-38 (1994)

MEDLINE  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

94150718  
2 (bases 1 to 30911)

Gardner, A.  
Direct Submission  
Submitted (19-APR-1996) Louis, MO 63110, USA. E-mail:  
jess@sanger.ac.uk or tw@nemastode.wustl.edu

Coding sequences below are predicted from computer analysis, using  
predictions from GeneFinder (P. Green, U. Washington), and other  
available information.  
For a graphical representation of this sequence and its analysis  
see:-  
http://web.archive.org/web/19960419000000/http://www.sanger.ac.uk/cgi-bin/display?db=wormace&class=Sequence&object=R06C7

Current sequence finishing criteria for the C. elegans genome  
sequencing consortium are that all bases are either sequenced  
unambiguously on both strands, or on a single strand with both a  
dye primer and dye terminator reaction, from distinct subclones.  
Exceptions are indicated by an explicit note.  
IMPORTANT: This sequence is NOT necessarily the entire insert of  
the specified clone. It may be shorter because we only sequence  
overlapping sections once, or longer because we arrange for a small  
overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone R06C7.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.

The true left end of clone R06C7 is at 1 in this sequence. The true  
right end of clone R06C7 is at 8718 in  
sequence Z71261.  
The true left end of clone F21C3 is at 30808 in this sequence. The  
start of this sequence (1..106) overlaps with the end of sequence  
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FEATURES  
source

gene

CDS

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